

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/801,486A
Source: JFW/6
Date Processed by STIC: 9/28/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/28/2006

PATENT APPLICATION: US/10/801,486A

TIME: 08:50:34

Input Set : A:\00281bus.txt

Output Set: N:\CRF4\09282006\J801486A.raw

4 <110> APPLICANT: Yan, Riqiang
 5 Tomasselli, Alfredo G.
 6 Gurney, Mark E.
 7 Emmons, Thomas L.
 8 Bienkowski, Mike J.
 9 Heinrikson, Robert L.
 11 <120> TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
 13 <130> FILE REFERENCE: 29915/00281BUS
 15 <140> CURRENT APPLICATION NUMBER: 10/801,486A
 16 <141> CURRENT FILING DATE: 2004-03-16
 18 <150> PRIOR APPLICATION NUMBER: 09/908,943
 19 <151> PRIOR FILING DATE: 2001-07-19
 21 <150> PRIOR APPLICATION NUMBER: 60/219,795
 22 <151> PRIOR FILING DATE: 2000-07-19
 24 <160> NUMBER OF SEQ ID NOS: 199
 26 <170> SOFTWARE: PatentIn Ver. 2.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 2070
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
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 35 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctggggg 120
 36 ctgcggtgctg cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
 37 gtggagatgg tggacaacct gaggggcaag tgggggcagg gctactacgt ggagatgacc 240
 38 gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
 39 gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
 40 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
 41 ctgggcaccg acctggtaag catcccccat ggccccaacg tctactgtgc tgccaacatt 480
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 43 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
 44 ctgggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660
 45 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720
 46 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780
 47 gaggtcatca ttgtgagggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
 48 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
 49 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
 50 ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
 51 ttcccagtc tctactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
 52 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
 53 tacaagtttg ccatctcaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1200
 54 ggcttctacg ttgtctttga tcggggccga aaacgaattg gctttgctgt cagcgttgc 1260
 55 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320

(Pg. 6-7)

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56 gaagactgtg gctacaacat tccacagaca gatgagtcaa cctcatgac catagcctat 1380
57 gtcattggtg ccatctgcgc cctcttcatg ctgccactct gcctcatggt gtgtcagtgg 1440
58 cgctgcctcc gctgcctgcg ccagcagcat gatgactttg ctgatgacat ctccctgctg 1500
59 aagtgaggag gcccatgggc agaagataga gattccccctg gaccacacct ccgtggttca 1560
60 ctttggtcac aagtaggaga cacagatggc acctgtggcc agagcacctc aggaccctcc 1620
61 ccaccacca aatgcctctg ccttgatgga gaaggaaaag gctggcaagg tgggttccag 1680
62 ggactgtacc tgtaggaaac agaaaagaga agaaagaagc actctgctgg cgggaatact 1740
63 cttggtcacc tcaaatttaa gtcgggaaat tctgctgctt gaaacttcag ccctgaacct 1800
64 ttgtccacca ttcttttaa ttctccaacc caaagtattc ttcttttctt agtttcagaa 1860
65 gtactggcat cacacgcagg ttaccttggc gtgtgtccct gtggtaccct ggcagagaag 1920
66 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
67 tgcttttagag acagggactg tataaacaag cctaacattg gtgcaaagat tgcctcttga 2040
68 attaaaaaaaa aaaaaaaaaa aaaaaaaaaa                2070

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70 <210> SEQ ID NO: 2

71 <211> LENGTH: 501

72 <212> TYPE: PRT

73 <213> ORGANISM: Homo sapiens

75 <400> SEQUENCE: 2

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79 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
80 20 25 30
82 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
83 35 40 45
85 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
86 50 55 60
88 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
89 65 70 75 80
91 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
92 85 90 95
94 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
95 100 105 110
97 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
98 115 120 125
100 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
101 130 135 140
103 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
104 145 150 155 160
106 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
107 165 170 175
109 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
110 180 185 190
112 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
113 195 200 205
115 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
116 210 215 220
118 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
119 225 230 235 240
121 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg

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122          245          250          255
124 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
125          260          265          270
127 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
128          275          280          285
130 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
131          290          295          300
133 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
134 305          310          315          320
136 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
137          325          330          335
139 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
140          340          345          350
142 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
143          355          360          365
145 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
146          370          375          380
148 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
149 385          390          395          400
151 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
152          405          410          415
154 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
155          420          425          430
157 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
158          435          440          445
160 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
161          450          455          460
163 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
164 465          470          475          480
166 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
167          485          490          495
169 Ile Ser Leu Leu Lys
170          500
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 1977
175 <212> TYPE: DNA
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 3
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181 ctgcggtctg cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
182 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
183 gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
184 gtgggtgctg cccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
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186 ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480
187 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatacct 540
188 gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct 600
189 gaagtgtctg cctctgtcgg agggagcatg atcattggag gtatcgacca ctgcgtgtac 660

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192 agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca 840
193 gtcaaatacca tcaaggcagc ctctccacag gagaagttcc ctgatggttt ctggctagga 900
194 gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcattctca 960
195 ctctacctaa tgggtgaggt taccaaccag tccttccgca tcaccatcct tccgcagcaa 1020
196 tacctgcggc cagtgggaaga tgtggccacg tcccaagacg actggtacaa gtttgccatc 1080
197 tcacagtcac ccacgggcac tgttatggga gctgttatca tggagggcct ctacgttgctc 1140
198 tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
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203 tgggcagaag atagagattc ccctggacca cacctccgtg gttcactttg gtcacaagta 1500
204 ggagacacag atggcacctg tggccagagc acctcaggac cctccccacc caccaaatac 1560
205 ctctgccttg atggagaagg aaaaggctgg caaggtgggt tccagggact gtacctgtag 1620
206 gaaacagaaa agagaagaaa gaagcactct gctggcgagg atactcttgg tcacctcaaa 1680
207 ttaaagtcgg gaaattctgc tgcttgaaac ttcagccctg aacctttgtc caccattcct 1740
208 ttaaattctc caacccaaag tattcttctt ttcttagttt cagaagtact ggcatcacac 1800
209 gcaggttacc ttggcgtgtg tccctgtggg acctggcagc agaagagacc aagcttggtt 1860
210 ccctgctggc caaagtcagt aggagaggat gcacagtttg ctatttgctt tagagacagg 1920
211 gactgtataa acaagcctaa cattggtgca aagattgcct cttgaaaaaa aaaaaaa 1977

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213 <210> SEQ ID NO: 4

214 <211> LENGTH: 476

215 <212> TYPE: PRT

216 <213> ORGANISM: Homo sapiens

218 <400> SEQUENCE: 4

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223           20           25           30
225 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
226           35           40           45
228 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
229           50           55           60
231 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
232           65           70           75           80
234 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
235           85           90           95
237 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
238           100          105          110
240 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
241           115          120          125
243 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
244           130          135          140
246 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
247           145          150          155          160
249 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
250           165          170          175

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252 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
253           180           185           190
255 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
256           195           200           205
258 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
259       210           215           220
261 Trp Tyr Thr Pro Ile Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
262 225           230           235           240
264 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
265           245           250           255
267 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
268           260           265           270
270 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
271           275           280           285
273 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
274       290           295           300
276 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
277 305           310           315           320
279 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
280           325           330           335
283 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
284           340           345           350
286 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
287           355           360           365
289 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
290       370           375           380
292 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
293 385           390           395           400
295 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
296           405           410           415
298 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
299           420           425           430
301 Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
302       435           440           445
304 Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
305       450           455           460
307 His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
308 465           470           475
311 <210> SEQ ID NO: 5
312 <211> LENGTH: 14
313 <212> TYPE: PRT
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
318     peptide sequence
320 <400> SEQUENCE: 5
321 Lys Val Glu Ala Asn Tyr Glu Val Glu Gly Glu Arg Lys Lys
322   1           5           10
325 <210> SEQ ID NO: 6

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/801,486A

DATE: 09/28/2006
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Input Set : A:\00281bus.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 7
Seq#:15; Xaa Pos. 4,7
Seq#:16; Xaa Pos. 1,4,5,6,7
Seq#:17; Xaa Pos. 1,2,4,5,6,7
Seq#:18; Xaa Pos. 1,2,4,5,6,7
Seq#:21; Xaa Pos. 5
Seq#:27; Xaa Pos. 7,19
Seq#:28; Xaa Pos. 6,7,11,20
Seq#:41; Xaa Pos. 9
Seq#:49; Xaa Pos. 1
Seq#:50; Xaa Pos. 2
Seq#:51; Xaa Pos. 3
Seq#:52; Xaa Pos. 4
Seq#:53; Xaa Pos. 5
Seq#:54; Xaa Pos. 6
Seq#:55; Xaa Pos. 7
Seq#:56; Xaa Pos. 8
Seq#:57; Xaa Pos. 1
Seq#:58; Xaa Pos. 2
Seq#:59; Xaa Pos. 3
Seq#:60; Xaa Pos. 4
Seq#:61; Xaa Pos. 5
Seq#:62; Xaa Pos. 6
Seq#:63; Xaa Pos. 7
Seq#:64; Xaa Pos. 8
Seq#:65; Xaa Pos. 1
Seq#:66; Xaa Pos. 2
Seq#:67; Xaa Pos. 3
Seq#:68; Xaa Pos. 4
Seq#:69; Xaa Pos. 5
Seq#:70; Xaa Pos. 6
Seq#:71; Xaa Pos. 7
Seq#:72; Xaa Pos. 8
Seq#:73; Xaa Pos. 1
Seq#:74; Xaa Pos. 2
Seq#:75; Xaa Pos. 3
Seq#:76; Xaa Pos. 4
Seq#:77; Xaa Pos. 7
Seq#:78; Xaa Pos. 8
Seq#:79; Xaa Pos. 8
Seq#:80; Xaa Pos. 9
Seq#:81; Xaa Pos. 1,7
Seq#:82; Xaa Pos. 2,7
Seq#:83; Xaa Pos. 3,7

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Input Set : A:\00281bus.txt
Output Set: N:\CRF4\09282006\J801486A.raw

Seq#:84; Xaa Pos. 4,7
Seq#:85; Xaa Pos. 5,7
Seq#:86; Xaa Pos. 6,7
Seq#:87; Xaa Pos. 7
Seq#:88; Xaa Pos. 7,8
Seq#:89; Xaa Pos. 1
Seq#:90; Xaa Pos. 1,2

VERIFICATION SUMMARY

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L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:595 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1045 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:1064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
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L:1197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
L:1216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:0
L:1273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
L:1292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:0
L:1311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0
L:1349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0
L:1368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0
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L:1521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0
L:1540 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0
L:1559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
L:1578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:0
L:1597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:0
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:1635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:0
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
L:1683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
L:1707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
L:1731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
L:1755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0

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Output Set: N:\CRF4\09282006\J801486A.raw

L:1779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0

L:1798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0